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(71)(72) Applicants and Inventors: KARAPLIS, Andrew, C. [CA/CA]; 95 Meaney, Kirkland, Quebec H9J 3V6 (CA). GOLTZMAN, David [CA/CA]; 667 Belmont, Westmount, Quebec H3Y 2W3 (CA). HENDERSON, Janet, E. [CA/CA]; 70 Woseley, Montreal West, Quebec H4X 1V7 (CA). LIPMAN, Mark, L. [CA/CA]; 2258 Fulton Road, Town of Mount Royal, Quebec H3R 2L4 (CA). PANDA, Dibyendu [IN/CA]; 3721 Dupuis, Montreal, Quebec H3T 1E5 (CA). SHEN, Yingnian [CA/CA]; 3870 Barclay, Montreal, Quebec H3S 1K7 (CA).			
(74) Agent: COTE, France; Swabey Ogilvy Renault, Suite 1600, 1981 McGill College Avenue, Montreal, Quebec H3A 2Y3 (CA).			

(54) Title: CLONING OF FULL-LENGTH HUMAN PEX cDNA

(57) Abstract

The present invention relates to the cloning of full-length human PEX cDNA isolated from tumors causing oncogenous hypophosphatemia osteomalacia, uses of PEX active site for the design of drugs to inhibit protein activity in cases of hypophosphatemia or chronic renal failure, uses of the PEX active site as a target for the treatment of hypophosphatemia or chronic renal failure and uses in the diagnosis of hypophosphatemia or chronic renal failure, use of PEX for the design of drugs to inhibit protein activity in cases of hypophosphatemia or chronic renal failure, use of PEX as a target for the treatment of hypophosphatemia, chronic renal failure, hypophosphatemia or idiopathic hypercalcuria, and use of PEX in the diagnosis of hypophosphatemic states, chronic renal failure, hypophosphatemic states or idiopathic hypercalcuria.

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CLONING OF FULL-LENGTH HUMAN PEX cDNA

BACKGROUND OF THE INVENTION5 (a) Field of the Invention

The invention relates to the cloning of full-length human PEX cDNA isolated from tumors causing oncogenous hypophosphatemia osteomalacia, uses of PEX active site for the design of drugs to inhibit protein 10 activity in cases of hyperphosphatemia or chronic renal failure, uses of the PEX active site as a target for the treatment of hyperphosphatemia or chronic renal failure and uses in the diagnosis of hyperphosphatemia or chronic renal failure, use of PEX for the design of 15 drugs to inhibit protein activity in cases of hyperphosphatemia or chronic renal failure, use of PEX as a target for the treatment of hyperphosphatemia, chronic renal failure, hypophosphatemia or idiopathic hypercalcuria, and use of PEX in the diagnosis of hyperphosphatemic states, chronic renal failure, hypophosphatemic states or idiopathic hypercalcuria.

20 (b) Description of Prior Art

Oncogenous hypophosphatemic osteomalacia (OHO) 25 is a rare acquired disease characterized by severe hypophosphatemia, inappropriate phosphaturia, reduced vitamin D levels, and defective bone mineralization (Ryan, E.A. and Reiss, E., 1984, *The American Journal of Medicine*, 77:501-512). This syndrome is associated 30 with a variety of histologically distinct, usually benign, mesenchymal tumors. Resection of the tumor reverses the metabolic abnormalities and results in cure of the bone disease. It has been postulated that a phosphaturic factor produced by these tumors promotes 35 the renal phosphate loss, which in turn results in osteomalacia. The putative phosphaturic factor may also

inhibit the renal conversion of 25-hydroxyvitamin D3 to 1,25-dihydroxy-vitamin D3. Depressed 1,25-dihydroxyvitaminD3 levels and chronic phosphate depletion may act synergistically to produce osteomalacia in these patients. The nature of the phosphaturic substance remains unknown and is distinct from parathyroid hormone and calcitonin, two polypeptide hormones known to inhibit the tubular reabsorption of phosphorus.

X-linked hypophosphatemia (HYP) is an inherited disorder of phosphate homeostasis with biochemical and physical findings very similar to OHO (Scriver, C.R. and Tenenhouse, H.S., 1992, *J. Inher. Metab. Dis.*, 15:610-624). By positional cloning, a gene which spans the deleted region Xp22.1 in HYP patients, or is mutated in non-deletion patients has been identified and its partial cDNA sequence reported. This gene exhibits homology to a family of endopeptidase genes involved either in activation or degradation of a number of peptide hormones and has been named PEX (phosphate regulating gene with homologies to endopeptidases, on the X chromosome) (The HYP Consortium, 1995, *Nature Genetics*, 11:130-136).

It would be highly desirable to be provided with a means to inhibit protein activity in cases of hyperphosphatemia, to be provided with a target for the treatment of hyperphosphatemia and to be provided with a diagnostic tool for hyperphosphatemic states.

SUMMARY OF THE INVENTION

One aim of the present invention is to employ the PEX active site of the design of drugs to inhibit protein activity in cases of hyperphosphatemia.

Another aim of the present invention is to employ the PEX active site as a target for the treatment of hyperphosphatemic or hypophosphatemic disorders

such as chronic renal failure, or idiopathic hypercalcuria, respectively.

Another aim of the present invention is to employ the PEX active site in the diagnosis of hyperphosphatemic and hypophosphatemic disorders.

The availability of full length PEX cDNA provides us with an unprecedented opportunity to study the biology of PEX and evaluate its role in conditions such as OHO, idiopathic hypercalcuria, HYP (a hypophosphatemic disorder) and in common pathological states characterized by impaired phosphate excretion including the large and expanding population of patients with chronic renal failure.

In accordance with the present invention there is provided a recombinant PEX protein generated from cloned cDNA depicted in Figs. 1A to 1G.

In accordance with the present invention there is provided a polyclonal or monoclonal antibody raised against the PEX active site which consists of at least amino acid residue 579 to residue 749 illustrated in Figs. 1A to 1G.

In accordance with the present invention there is provided a method for the design of drugs to be used as competitive inhibitors or activators of PEX enzymatic activity and/or its receptor in cases of hyperphosphatemia (as in chronic renal failure) or hypophosphatemia, which comprises the steps of:

- a) developing a radiolabeled or fluorescent-labeled metalloendopeptidase substrate which reversibly or irreversibly binds PEX; and
- b) using PEX and the labeled ligand to screen an expression library for an endogenous protein which binds PEX;

or

-using labeled PEX to examine its competitive binding to a receptor;

or

5 -using labeled recombinant PEX to screen an expression library in order to clone its receptor.

In accordance with the present invention there is provided a method for the treatment of hyperphosphatemia or of chronic renal failure which comprises 10 administering to a patient an effective amount of a pharmaceutical compound targeted to inhibit PEX active site and/or its receptor.

In accordance with the present invention there is provided a method for the diagnosis of hyperphosphatemic or hypophosphatemic conditions in patient, 15 which comprises the steps of :

- a) preparing a solid support having bound thereto at least one of the anti-PEX antibody of the present invention, the recombinant PEX protein of the present 20 invention, or the active site thereof;
- b) screening a biological sample of the patient on the solid support; and
- c) detecting the presence of PEX protein or PEX antibody in the sample, thereby indicating the presence 25 of hyperphosphatemic or hypophosphatemic conditions.

In accordance with the present invention there is provided a transgenic mouse in which the wild type and mutant PEX cDNA depicted in Figs. 1A to 1G has been inserted into the murine genome to cause alterations in 30 blood and urine phosphate and the murine counterpart of HYP and OHO. Such a transgenic mouse may be used to study the biology of PEX protein in vivo and its ability to reverse biochemical and physical abnormalities 35 associated with HYP in mice and patients in the form of gene therapy.

In accordance with the present invention there is provided a method for the treatment of cancer which comprises determining the role of PEX in tumor growth by assessing its activity and/or prenylation during 5 neoplastic transformation and using drug design to create novel anticancer treatments which interfere with PEX protein function.

BRIEF DESCRIPTION OF THE DRAWINGS

10 Figs. 1A-1G illustrate the nucleotide sequence and predicted amino acid sequence of tumor PEX cDNA;

15 Figs. 2A-2C illustrate the amino acid homology between PEX and human NEP cDNA with the sequence comparison performed by LALIGN (a computer program designed to maximally align two different protein sequences); and

Fig. 3 illustrates the hydropathy plot of PEX cDNA.

20 **DETAILED DESCRIPTION OF THE INVENTION**

In accordance with the present invention, PEX expression in tumors associated with the syndrome (OHO) was examined.

25 We have used the PCR technique to clone and characterize full-length human PEX cDNA from two tumors associated with OHO and have determined its normal fetal and adult tissue distribution. We show that full-length human PEX cDNA encodes a 749 amino acid protein (Figs. 1A-1G) with extensive homology to the human neutral endopeptidase (Fig. 2) (NEP; EC 3.4.24.11), suggesting that PEX is a metalloendopeptidase. The additional sequences provided by our PEX cDNA clone include 30 603 nucleotides of the 5' noncoding region, the first 3 and the last 108 amino acids of the protein, comprising 35 residues postulated to be critical for the formation of

the active site of the protein and hence its enzymatic activity, the termination codon, as well as 276 nucleotides of the 3' noncoding region, including the polyadenylation signal. We also show that PEX has a 5 cleavable signal sequence and a consensus sequence for prenylation of the protein at its carboxyl terminal.

In summary, the cloning of the full-length human PEX cDNA from tumors causing OHO is reported in the present invention. The availability of this cDNA opens 10 new and exciting avenues of investigation in a number of clinical specialties, such as endocrinology, nephrology, and oncology. The biology of PEX will be evaluated in conditions such as OHO, idiopathic hypercalcuria, and HYP.

15

Tumor Tissues

Tumor tissues were removed from two patients with well-documented OHO. Resection of the tumors resulted in the complete reversal of the biochemical 20 and physical abnormalities associated with the syndrome. Tumor tissue was frozen immediately in liquid nitrogen and stored at -70°C.

25 PEX Expression in OHO-associated tumors

To determine whether PEX is expressed in tumors associated with OHO, RNA was extracted from tumor tissue using Qiagen RNeasy Kit™ and reversed transcribed using oligodT primer and Superscript II (BRL) reverse transcriptase for 1 hour at 42°C in a final reaction 30 volume of 30 µl. The resulting cDNA was then amplified using human PEX-specific primers, PEX 1 (5' GGAGGAATTGGTTGAGGGCG 3') and PEX 2 (5' GTAGACCACCAAGGATCCAG 3'). Following amplification (35 cycles) the PCR reaction was fractionated on a 1% agarose gel stained with ethidium bromide. PEX mRNA was 35 readily amplified from both samples demonstrating the

expected 509 bp amplified fragment, as predicted from the published partial sequence.

Cloning of full-length PEX cDNA from tumors

5 Cloning of the 5' end of PEX cDNA was accomplished by anchored PCR. Total cellular RNA was initially extracted from tumor tissue followed by the isolation of mRNA. 1.5 μ g of mRNA was then reverse transcribed into cDNA using 200 ng of a PEX specific 10 antisense oligomer (PEX 2) and 200 units of Superscript II (BRL) reverse transcriptase for 1 hour at 42°C in a final reaction volume of 30 μ l. The resulting cDNA was size fractionated on a 1% agarose gel and fragments corresponding to >600 bp were purified and resuspended 15 in H₂O. The 3' end of the first strand cDNA was homopolymer tailed with dGTP using 1 μ l of Terminal deoxynucleotidyl transferase (TdT) at 37°C for 30 minutes in a volume of 50 μ l. Following heat inactivation of the enzyme, RNA template was removed by incubation with RNase H and the tailed cDNA was purified by 20 phenol-chloroform extraction followed by ammonium acetate precipitation. The purified tailed cDNA was resuspended in H₂O and an aliquot was used for anchored PCR along with 200 ng of an internal PEX specific antisense 25 primer (PEX 3, 5' CGTGCCCAGAACTAGGGTGCCACC 3') and 200 ng of oligo(dC) as the sense primer. Forty cycles of PCR were performed using 0.5 μ l of Taq polymerase (Promega) in a reaction volume of 50 μ l. Cycling parameters were: 1 minute of denaturation at 95°C, 2 minutes of 30 annealing at 55°C and 2 minutes of extension at 72°C. The PCR products were fractionated on a 1% agarose gel and a band of 700 bp was isolated, purified, and ligated into pPCRTM II vector (Invitrogen). Following 35 transformation into HB101 bacteria, clones containing the appropriate size insert were sequenced using Sequenase kit (US Biochem).

To clone the 3' end of PEX cDNA, an aliquot of an amplified unidirectional cDNA library in pCDNA3 vector (Invitrogen) generated from tumor mRNA was grown overnight in LB medium and plasmid DNA extracted. DNA 5 (0.5 µg) was subjected to PCR using a PEX-specific sense oligomer (PEX1) and an antisense oligomer corresponding to SP6 RNA polymerase binding site sequences present in the pCDNA3 vector. Thirty five cycles of amplification were performed in a 50 µl reaction volume 10 with each cycle consisting of 1 min. denaturation at 94°C, 1 min. annealing at 55°C and 1 min. extension at 72°C. Amplified products were fractionated on a 1% agarose gel and a 1.2 kb fragment corresponding to the 3' end of PEX cDNA was subcloned and sequenced.

15 Figs. 1A-1G show the nucleotide and predicted amino acid sequence of the full-length PEX cDNA cloned from tumor tissue. In both tumors, there were three amino acids that differ from the published partial PEX sequence, 363_D->A(GAC to GCC), 403_R->W(AGG to TGG), and 20 641_A->G(GCG to GGA). Full-length human PEX cDNA encodes 749 amino acids and has extensive homology to the human neutral endopeptidase (Fig. 2) (NEP; EC 3.4.24.11), suggesting that PEX is a metalloendopeptidase. The additional sequences provided by our PEX cDNA clone 25 include 603 nucleotides of the 5' noncoding region, as well as the first 3 and the last 108 amino acids of the protein. These additional amino acids comprise residues that may be critical for the formation of the active site of the protein and hence its enzymatic activity, 30 such as 642_E, 710_H, and 693,733,746_C. Our PEX clone also identifies the termination codon, as well as 276 nucleotides of the 3' noncoding region, including the polyadenylation signal. Hydropathy plot and PSORT analysis of the PEX protein identified a putative 35 cleavable signal sequence composed of the first 49

amino acids, implicating amino acid 50 at the beginning of the mature protein (Fig. 3). This contrasts with the human NEP sequence that does not have a cleavable signal sequence. PEX protein has also been shown to 5 have a carboxyl terminal motif (CAAX box: CRLW) that may direct prenylation of the protein, a post-translational modification that may be important in neoplastic processes, and could be targeted for pharmacological manipulation.

10 Northern-blot analysis

Total RNA was prepared from human Saos-2 osteosarcoma cells by Trizol™ and polyA+ RNA was isolated using standard procedures. Twenty micrograms of 15 PolyA+ RNA were fractionated on 1% denaturing agarose gel, transferred to nylon membrane and probed with ³²P-labeled human PEX cDNA. The blot was washed in 0.1 X SSC at 55°C for 20 min., and subjected to autoradiography for 7 days. To monitor loading, the membrane was 20 re-probed with an GAPDH cDNA probe. In these cells, a single weak transcript was detected with mobility slightly faster than 28S RNA, consistent with the predicted size from the cloned PEX cDNA (~3.1 kb) and a more intense signal was observed of ~6.6 kb size.

25 Tissue Distribution of PEX mRNA

Recent studies have not documented the presence 30 of PEX mRNA in normal tissues except for fetal brain and human leukocytes (The HYP Consortium, 1995, *Nature Genetics*, 11:130-136). Following the cloning of full-length PEX, we examined PEX expression in normal fetal and adult tissues and in a number of established human cell lines using RT-PCR. PEX was found to be expressed 35 in fetal calvarium (bone) and to a lesser degree in fetal kidney and muscle while no expression was apparent in fetal liver. In adult tissues, PEX mRNA was identified in kidney, but not in liver, or endomyocard-

dium. Interestingly, weak expression was evident in tissue from an atrial myxoma, a tumor of mesenchymal origin and in renal cell carcinoma, an epithelial tumor. A number of established human cell lines were 5 also shown to express PEX, including the Saos-2 osteosarcoma cells.

In vitro transcription and translation

Plasmid pPEX was linearized at the XhoI site of 10 the polylinker region and sense RNA strand was transcribed using T7 RNA polymerase. Translation reactions in rabbit reticulocyte lysate were performed according to the manufacturer's (Promega) procedure either in the absence or presence of canine pancreas microsomal membranes. Samples were processed for SDS-polyacrylamide 15 gel electrophoretic (PAGE) analysis of the peptides, and autoradiography were performed. In the absence of microsomal membranes, PEX cRNA was translated into a ~82kD protein. Following the addition of microsomal 20 membranes, two translated products of higher molecular weight were apparent, consistent with N-glycosylation of PEX (nine potential sites).

The present invention will be more readily understood by referring to the following examples which 25 are given to illustrate the invention rather than to limit its scope.

EXAMPLE I

Uses of recombinant PEX protein

Recombinant PEX protein will be generated from 30 the cloned cDNA and an assay will be developed to clone the PEX substrate and/or PEX receptor which may also have important biological functions. For this assay, a soluble form of PEX protein will be used to bind a fluorescent substrate and conditioned media from COS 35 cells transfected with various cDNA expression libraries will be used to compete with the substrate for the

PEX protein. Step-wise analysis will lead to identification of the cDNA encoding the physiological substrate of PEX. Other studies will determine if radiolabeled recombinant PEX interacts with a specific receptor and 5 if so, the receptor will be cloned by expression cloning.

EXAMPLE II
Uses of specific anti-PEX antibody

Specific PEX antibodies will be generated for 10 developing assays that will measure circulating levels of this peptide in various clinical states such as chronic renal failure.

EXAMPLE III
Competitive inhibitors or activators of PEX enzymatic activity

Other studies will concentrate on the role of PEX in common pathological states characterized by impaired phosphate excretion, as in patients with 20 chronic renal failure. These patients develop hyperphosphatemia that causes a number of complications such as ectopic calcifications, secondary hyperparathyroidism and inevitable metabolic bone disease leading to increased morbidity and mortality. The potential 25 therapeutic value of pharmacological manipulation of PEX in this condition will be examined by designing competitive inhibitors or activators of its enzymatic activity and/or its receptor, and studying their effects, first in animal models of chronic renal failure, 30 and eventually in patients.

EXAMPLE IV
Gene transfer using PEX cDNA

In animal studies, we will use the technique of 35 gene transfer to introduce normal and mutated PEX cDNA in normal mice and in mice with the murine counterpart of HYP to study the biology of the protein and its

ability to reverse the biochemical and physical abnormalities associated with the latter disorder. Potentially, these experiments can be extended for therapeutic purposes to patients with HYP as well as other 5 disorders of phosphate homeostasis.

EXAMPLE V
Role of PEX in tumors

Finally, studies will also be directed in 10 defining the role of PEX in tumor growth by assessing its activity and/or prenylation during neoplastic transformation. Prenylation is necessary for association with the plasma membrane and cell transformation. The critical role of prenylation can be exploited by 15 the use of rational drug design to create novel anti-cancer treatments that interfere with PEX protein function.

While the invention has been described in connection with specific embodiments thereof, it will be 20 understood that it is capable of further modifications and this application is intended to cover any variations, uses, or adaptations of the invention following, in general, the principles of the invention and including such departures from the present disclosure 25 as come within known or customary practice within the art to which the invention pertains and as may be applied to the essential features hereinbefore set forth, and as follows in the scope of the appended claims.

WE CLAIM:

1. Recombinant PEX protein generated from cloned cDNA depicted in Figs. 1A to 1G.
2. A polyclonal or monoclonal antibody raised against the PEX active site which consists of at least amino acid residue 579 to residue 749 illustrated in Figs. 1A to 1G.
3. A method for the design of drugs to be used as competitive inhibitors or activators of PEX enzymatic activity and/or its receptor in cases of hyperphosphatemia (as in chronic renal failure) or hypophosphatemia, which comprises the steps of:
 - a) developing a radiolabeled or fluorescent-labeled metalloendopeptidase substrate which reversibly or irreversibly binds PEX; and
 - b) using PEX and said labeled ligand to screen an expression library for an endogenous protein which binds PEX;

or

using labeled PEX to examine its competitive binding to a receptor;

or

using labeled recombinant PEX of claim 1 to screen an expression library in order to clone its receptor.
4. A method for the treatment of hyperphosphatemia or of chronic renal failure which comprises administering to a patient an effective amount of a pharmaceutical compound targeted to inhibit PEX active site and/or its receptor.

5. A method for the diagnosis of hyperphosphatemic or hypophosphatemic conditions in patient, which comprises the steps of :

- a) preparing a solid support having bound thereto at least one of the antibody of claim 2, the recombinant PEX protein of claim 1, or the active site thereof;
- b) screening a biological sample of the patient on said solid support; and
- c) detecting the presence of PEX protein or PEX antibody in said sample, thereby indicating the presence of hyperphosphatemic or hypophosphatemic conditions.

6. A transgenic mouse in which the wild type and mutant PEX cDNA depicted in Figs. 1A to 1G has been inserted into the murine genome to cause alterations in blood and urine phosphate in the murine counterpart of HYP and OHO.

7. The use of the mouse of claim 6 to study the biology of PEX protein in vivo and its ability to reverse biochemical and physical abnormalities associated with HYP in mice and patients in the form of gene therapy.

8. A method for the treatment of cancer which comprises determining the role of PEX in tumor growth by assessing its activity and/or prenylation during neoplastic transformation and using drug design to create novel anticancer treatments which interfere with PEX protein function.

1 GAT CCA CTA GTA ACG GCC GCG AGT GTG GTG GAA TTC AAG GGA CTC ACA CAC TGA AAG ATT
61 ATC TTT GAT GAA GAC AAT TCA GGC AAG CAG AAT GAT TCT TGC AAC AGA ATT ACA TGA TTA
121 ATT GAG ATC TTG AAG TGG GTC CGG TGA ATC CTG GCC ACC TAA CTT ATC ATG ATT TGG GGG
181 AGT TTC ACG AGA ATC CAG TTT TGA TAA AAC AAT TGT TTT CCT CCC CAA GTG ACT ATA
241 CAT TTA AAT AGC TAA AAC ATC TGT TCA GCA ACA TAG TAA AAC ATA TAT ACT CGG AAC GCT
301 TGA GAG AAG AGC CTG CCA AAC AGG GAC TTT GCT GAG GGA GAG CAC CAA GAT AAA GCA ACA
361 CTG TTT GTT TTG TCT AGT CAG GGG GGA AAG CCA AGG CAA CCA ATA TTT TGG TTT TTA TAA
421 TTT TCA TTT GTG AAG AAT TAT TTG AGA AAG GGT TGG CGA GGG GAG ATT TCC TGA CGG CAG
481 TTT CTT AAG CTG TCC ATT AGT AGA AGA GCA AGA GAG CCT TGG ATG TCA ACG CCT CGC TCT
541 TGA GAC CAG CCA CCA AAC AAC CAC GAA AAG **TGA** CTT TCT CGT GTG CTC TCT ACG GCC CTT
601 /1 631/10

1/11

7 8 9 - 1A

CTG ATG GAA GCA GAA ACA GGG AGC AGC GTG GAG ACT GGA AAG AAC GCC AGA GGC ACT
 M E A E T G S S V E T G K K A N R G T
 661/20 691/30
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 R I A L V V F V G G T L V L G T I L F L
 721/40 751/50
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 V S Q G L L S L Q A K Q E Y C L K P E C
 781/60 811/70
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 I E A A A I L S K V N L S V D P C D N
 841/80 871/90
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 1021/140 1051/150

2/11

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3/11

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 1141/180

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 1201/200

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 1261/220

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 1321/240

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 1381/260

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 1441/280

1471/290

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GTG GTC CGC GTC CCG CAG TAC TTT AAA GAT TTG TTG AGG ATA TTA GGG TCT GAG AGA AAG	V V R V P Q Y F K D L F R I L G S E R K	1621/340
AAG ACC ATT GAC AAC TAT TTG GTG TGG AGA ATG GTT TAT TCC AGA ATT CCA AAC CTT AGC	K T I D N Y L V W R M V Y S R I P N L S	1681/360
AGG CGC TTT CAG TAT AGA TGG CTG GAA TTC TCA AGG GTA ATC CAG GGG ACC ACA ACT TTC	R R F Q Y R W L E F S R V I Q G T T T L	1741/380
CTG CCT CAA AGG GAC AAA TGT GTA AAC TTT ATT GAA AGT GCC CTC CCT TAT GTT GTT GGI	L P Q R D K C V N F I E S A L P Y V V G	1801/400
1891/430		1831/410
1861/420		1771/390
1711/370		1651/350
1591/330		1531/310

SUBSTITUTE SHEET (RULE 26)

5/11

AAG ATG TTT GTA GAT GTG TAC TTC CAG GAA GAT AAG AAG GAA ATG ATG GAA TTT GTT	K M F V D V Y F Q E D K K E M M E E L V	1921/440
GAG GGC GTT CGC TGG GCC ATT GAC ATG CTA GAG AAA GAA AAT GAG TGG ATG GAT GCA	E G V R W A F I D M L E K E N E W M D A	1951/450
GGA ACG AAA AGG AAA GCC AAA GAA AAG GCG AGA GCT GTT TTG GCA AAA GTT GGC TAT CCA	G T K R K A K E K A R A V L A K V G Y P	1981/460
GAG TTT ATA ATG AAT GAT ACT CAT GTT AAT GAA GAC CTC AAA GCT ATC AAG TTT TCA GAA	E F I M N D T H V N E D L K A I K F S E	2041/480
GCC GAC TAC TTT GGC AAC GTC CTA CAA ACT CGC AAG TAT TTA GCA CAG TCT GAT TTC TTC	A D Y F G N V L Q T R K Y L A Q S D F F	2101/500
TGG CTA AGA AAA GCC GTT CCA AAA ACA GAG TGG TTT ACA AAT CCG ACG ACT GTC AAT GCC	W L R K A V P K T E W F T N P T T V N A	2161/520
		2221/540
TTC TAC AGT GCA TCC ACC AAC CAG ATC CGA TTT CCA GCA GGA GAG CTC CAG AAG CCT TTC	F Y S A S T N Q I R F P A G E L Q K P F	2281/560
		2311/570

~~7-1E~~ - 1E

6/11

TTT TGG GGA ACA GAA TAT CCT CGA TCT CTG AGT TAT GGT GCT ATA GGA GTA ATT GTC GGA
 F W G T E Y P R S L S Y G A I G V I V G

2341/580

CAT GAA TTT ACA CAT GGA TTT GAT AAT ATA GGT AGA AAA TAT GAT AAA AAT GGA AAC CTG
 H E F T H G F D N N G R K Y D K N G N L

2401/600

GAT CCT TGG TGG TCT ACT GAA TCA GAA GAA AAG TTT AAG GAA AAA ACA AAA TGC ATG ATT
 D P W W S T E S E E K F K E K T K C M I

2461/620

AAC CAG TAT AGC AAC TAT TAT TGG AAG AAA GCT GGC TTA AAT GTC AAG GGG AAG AGG ACC
 N Q Y S N Y Y W K K A G L N V K G K R T

2521/640

CTG GGA GAA AAT ATT GCT GAT AAT GGA GGC CTG CGG GAA GCT TTT AGG GCT TAC AGG AAA
 L G E N I A D N G G L R E A F R A Y R K

2581/660

TGG ATA AAT GAC AGA AGG CAG GGA CTT GAG GAG CCT CTT CTA CCA GGC ATC ACA TTC ACC
 W I N D R R Q G L E P L P G I T F T

2641/680

AAC AAC CAG CTC TTC CTG AGT TAT GCT CAT GTG AGG TGC AAT TCC TAC AGA CCA GAA
 N N Q L F F L S Y A H V R C N S Y R P E

2701/700

~~7-11~~ - 1F

7/11

GCT CGA GAA CAA GTC CAA ATT GGT GCT CAC AGT CCC CCT CAG TTT AGG GTC AAT GGT
A A R E Q V Q I G A H S P P Q F R V N G
2761/720 GCA ATT AGT AAC TTT GAA GAA TTC CAG AAA GCT TTT AAC TGT CCA CCC AAT TCC ACG ATG
A I S N F E E F Q K A F N C P P N S T M
2821/740 AAC AGA GGC ATG GAC TCC TGC CGA CTC TGG TAG CTG GGA CGC TGG TTT ATG GCA TCC TGA
N R G M D S C R L W * 2911
2881 GAC AGT TGC ACA GTG CCA GCG GAG GCT GCA CTG AGC CTT CAT CGC CCA TTG CTT TAG GCC
2941 TGG AGG AGC TTT CAT TTT TAG TGC ATT TTC ATT ATT TGG GTC GGT GAC CTG CTT GGA TCT
3001 AGA CAG CAT CTG TTC AAA GTT GTA GGG CTT ATA AAG TGG AAT ATA AGA AGA ACT AAG TAT
3061 GTT TCT TTA GAA AAT CAA ACC AAC AAA AAT AAA TCC CTA GGC TAC TTT TGT TAA AAA AAA
3121 AAA AAA AAA A

~~7/11~~ - 16

hPEX MEAETGSSVETGKKANRGTRIALVVVFVGGTLVLGTTILFLVSQGLLSQLQAKQEYCLKPECI
hNEP MESQMDITDINTPKPKKKQRWTPLEISLSVLLTIAVTMIALYATYDDGICKSSDCI

hPEX EAAAAILSKVNLSVDPACDGFNFRACDGFNFWIISNNNPIPEDMPSYGVYPWLRRHNVDLKLKELLE
hNEP KSAARLIIQNMDDATTEPCTDFFKYACGGWLKRNVIPEΤSSRYGNFDILRDELEVVLKDVLQ

hPEX KSISRRRDTEAIQKAKILYSSCMNEKAIEKADAKPLLHILRHSPPFRWPVLESNIGPEGVW
hNEP EPKT- -EDIVAVQKAKALYRSCINESAIDSRGGEPLLKLIPDI - YGWPVATENWEQKYGA

hPEX SERKFSLLQTLATFRGQYSNSVFIRLYVSPDDKASNEHILKLDQATLSSLAVREDYLDNST
hNEP SW---TAEKAIAQLN SKYGGKKVLINLFVGTDDKNSVNHVIHIDQPRRLGLPSRDYYECTGI

hPEX EAKSYRDALY - KFMVDTAVLLGANSRAEH - - - DMKSVLRLIEIKIAEIMIPHENRT - SE

8/11

~~7-11~~ - 2A

hNEP YKEACTAYVDFMISVARLIRQEERILPIDENQLALEMNVMELEKEIANATAKPEDRNDPM
 hPEX AMYNKMNISEL-SAMIPOQFDWLGYIK-KVIDTRLYPHLKDISPSENVVVRVPQYFKDLFR
 hNEP LLYNKMITLEAQI QNNFSLEINGKPF SWLNFTNEIMSTVNISITNEEDVVVVAPEYLTKLKP
 9/11
 hPEX ILGSERKKTIANYLWWRMIVYSRIPNLSSRRFQYRWRLEFSRVIQGTTTLLPQWDKCVNFILES
 hNEP ILTKYSARDLQNLMSWRFIMDLVSSLSRTYKESRNAFRKALYGTITSETATWRRRCANYVNG
 hPEX ALPYVVGKMFVVDVYFQEDKKEMMEELVEGVRWAFIDMLEKENEWMDAGTKRKAKEKARAV
 hNEP NMENAVGRLLYVEAAFAGESKHWVEDLIAQIREVFQTLD-DLTWMDAETKKRAEEKALAI
 hPEX LAKVGYPEFIM-NDTHVNEDLKA1KFSEADYFGNVLQTRKYLAQSDFFWLRKAVPKTEWF
 hNEP KERIGYPDDIVSNDNKLNNYELEYNYKEDEYFENIIQNLKFSQSOKQLKKLREKVDKDEWI
 hPEX TNPTTVNAFYSASTNQIRFPAGELOQKPEFWGTEYPRSLSYGA1GVIVGHEFTHGFDNNGR
~~75~~ - 2B

SGAAVNAFSSGRNQIVFPAGILQPPFESAQQSN - SLNYGGIGMVIGHETITHGFDNNGR
hNEP

KYDKNGNLDPMWSTSEEKFKEKTKCMINQYSNYYWKKAG - LNVKGKRTLGENIADNGGL
hPEX

NFNKDGLVWDWWTQQSASNFKEQSQCMVYQYGNFSWDLAGGQHNLNGINTLGENIADNGGL
hNEP

REAFRAYRKWINDRRQGLEEPLLPGITFTNNQLFFFLSYAHVR CNSYRPEAAREQVQIGAH
hPEX

GQAYRAYQ - - NYIKKNGEEKLLPGLDLNHKQLFFFLNFAQVWCGTYRPEYAVNSIKTDVH
hNEP

SPPQFRVNGAISNFEFFQKAFNCPPNSTMNRGMDSCRILW
hPEX

SPGNFRRIIGTLQNSAEFSEAFHCRKNSYMNPEKK - CRVW
hNEP

11/11

